

10/547206

SEQUENCE LISTING

DT09 Rec'd PCT/PTO 26 AUG 2005

<110> JACQUET, Alain

<120> HYPOALLERGENIC DER P1 AND DER P3 PROTEINS FROM DERMATOGRAPHOIDES
PTERONYSSINUS

<130> VB60107

<140> PCT/EP2004/001850
24-02-2004

<150> GB 0304424.5
26-02-2003

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 909

<212> DNA

<213> Dermatophagoides pteronyssinus

<220>

<221> CDS

<222> (1)...(906)

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aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe
20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc 192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag 240

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Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile	Asp	Leu	
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cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg															336	
Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly	Cys	Gly	
100															110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc															384	
Ser	Cys	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	
115															125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac															432	
Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp	
130															140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc															480	
Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile	
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Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr	
165															175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc															576	
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly	
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att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg															624	
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Ala	Asn	Lys	Ile	Arg	
195															205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc															672	
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	
210															220	
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Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	
225															240	
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt															768	
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly	
245															255	

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg	816		
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp			
260	265	270	
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc	864		
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile			
275	280	285	
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg	906		
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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
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Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
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Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
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Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg			

195	200	205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile		
210	215	220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln		
225	230	235
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly		
245	250	255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp		
260	265	270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile		
275	280	285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu		
290	295	300

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<220>
 <223> C4R mutant of ProDer p 1

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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	

Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly
180							185						190		
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg
195							200						205		
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile
210							215						220		
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln
225							230						235		240
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly
245							250						255		
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp
260							265						270		
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile
275							280						285		
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 <222> (1)...(906)

<223> C4R mutant of ProDer p 1

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 Arg¹ Pro² Ser³ Ser⁴ Ile⁵ Lys⁶ Thr⁷ Phe⁸ Glu⁹ Glu¹⁰ Tyr¹¹ Lys¹² Lys¹³ Ala¹⁴ Phe¹⁵ Asn¹⁶

a¹⁷ a¹⁸ g¹⁹ c²⁰ t²¹ g²² c²³ t²⁴ g²⁵ a²⁶ g²⁷ g²⁸ g²⁹ c³⁰ g³¹ c³² g³³ a³⁴ a³⁵ a³⁶ t³⁷ t³⁸ c³⁹ 96
 Lys¹ Ser² Tyr³ Ala⁴ Thr⁵ Phe⁶ Glu⁷ Asp⁸ Glu⁹ Glu¹⁰ Ala¹¹ Ala¹² Arg¹³ Lys¹⁴ Asn¹⁵ Phe¹⁶

c²⁰ t²¹ g²² a²³ g²⁴ a²⁵ g²⁶ t²⁷ g²⁸ a²⁹ a³⁰ c³¹ g³² g³³ g³⁴ g³⁵ c³⁶ t³⁷ a³⁸ t³⁹ a⁴⁰ a⁴¹ t⁴² c⁴³ a⁴⁴ c⁴⁵ 144
 Leu¹ Glu² Ser³ Val⁴ Lys⁵ Tyr⁶ Val⁷ Gln⁸ Ser⁹ Asn¹⁰ Gly¹¹ Gly¹² Ala¹³ Ile¹⁴ Asn¹⁵ His¹⁶

c⁵⁰ t⁵¹ c⁵² g⁵³ c⁵⁴ t⁵⁵ t⁵⁶ g⁵⁷ a⁵⁸ g⁵⁹ a⁶⁰ a⁶¹ c⁶² g⁶³ t⁶⁴ t⁶⁵ c⁶⁶ a⁶⁷ t⁶⁸ g⁶⁹ a⁷⁰ 192
 Leu¹ Ser² Asp³ Leu⁴ Ser⁵ Leu⁶ Asp⁷ Glu⁸ Phe⁹ Lys¹⁰ Asn¹¹ Arg¹² Phe¹³ Leu¹⁴ Met¹⁵ Ser¹⁶

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240		
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
acc aac gcc cgt agt atc aac ggc aat gcc ccc gct gag att gat ctg	288		
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	336		
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384		
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432		
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480		
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528		
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576		
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	624		
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg			
195	200	205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672		
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
210	215	220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720		
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln			
225	230	235	240
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt	768		
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly			

245	250	255	
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816			
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp			
260	265	270	
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864			
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile			
275	280	285	
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906			
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu			
290	295	300	
taa 909			
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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			

165	170	175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly		
180	185	190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg		
195	200	205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile		
210	215	220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln		
225	230	235
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly		
245	250	255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp		
260	265	270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile		
275	280	285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu		
290	295	300

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<223> C31R mutant of ProDer p 1

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 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1 5 10 15

a_ag ag_c tat g_cc acc tt_c gag g_ac gag g_ag g_cc g_cg a_ag a_ac tt_c 96
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
 20 25 30

ct_g gaa ag_c gt_g aaa tac gt_g cag ag_c a_ac g_gc g_gg g_ct ata a_at cac 144
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
 35 40 45

ct_g t_cc gac ct_g t_ct gac gag tt_c a_ag a_ac c_gg tt_c ct_g at_g ag_c 192
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
 50 55 60

gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240		
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	288		
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc cgt ggg	336		
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly			
100	105	110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384		
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432		
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480		
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528		
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576		
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	624		
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg			
195	200	205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672		
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
210	215	220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720		
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln			
225	230	235	240
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt	768		

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly			
245	250	255	
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg			816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp			
260	265	270	
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc			864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile			
275	280	285	
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg			906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu			
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taa			909
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Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
 165 170 175
 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
 180 185 190
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
 195 200 205
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
 210 215 220
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
 225 230 235 240
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
 245 250 255
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
 260 265 270
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
 275 280 285
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
 290 295 300

<210> 8
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(906)

<223> C65R mutant of ProDer p 1

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 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1 10 15

aag agc tat gcc acc ttc gag gac gag gag gcc gcg cgc aag aac ttc 96
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Ala Ala Arg Lys Asn Phe
 20 25 30

ctg gaa agc gtg aaa tac gtg cag agc aac ggc ggg gct ata aat cac 144
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
 35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cg₃₅ ttc ctg atg agc 192
 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser

50	55	60	
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag			240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg			288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg			336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc			384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac			432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
cgt gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc			480
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac			528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc			576
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg			624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg			
195	200	205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc			672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
210	215	220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag			720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln			
225	230	235	240

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt 768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
245 250 255

tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg 816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
260 265 270

gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc 864
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
275 280 285

gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg 906
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

taa 909

<210> 9
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> C71R mutant of ProDer p 1

<400> 9
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1 5 10 15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
20 25 30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
35 40 45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
50 55 60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65 70 75 80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
85 90 95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
115 120 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
130 135 140
Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile

145	150	155	160												
Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr
165															175
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly
180															190
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg
195															205
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile
210															220
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln
225															240
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly
245															255
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp
260															270
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile
275															285
Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu		
290															300

<210> 10
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(906)

<223> C71R mutant of ProDer p 1

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Arg	Pro	Ser	Ser	Ile	Lys	Thr	Phe	Glu	Glu	Tyr	Lys	Lys	Ala	Phe	Asn	
1				5						10					15	
aag	agc	tat	gcc	acc	ttc	gag	gac	gag	gag	gcc	gcg	cgc	aag	aac	ttc	96
Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	
20										25					30	
ctg	gaa	agc	gtg	aaa	tac	gtg	cag	agc	aac	ggc	ggg	gct	ata	aat	cac	144
Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	
35															45	
ctg	tcc	gac	ctg	tct	tta	gac	gag	ttc	aag	aac	cg	ttc	ctg	atg	agc	192

Leu	Ser	Asp	Leu	Ser	Leu	Asp	Glu	Phe	Lys	Asn	Arg	Phe	Leu	Met	Ser	
50			55				60									
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag															240	
Ala	Glu	Ala	Phe	Glu	His	Leu	Lys	Thr	Gln	Phe	Asp	Leu	Asn	Ala	Glu	
65			70				75									80
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg															288	
Thr	Asn	Ala	Cys	Ser	Ile	Asn	Gly	Asn	Ala	Pro	Ala	Glu	Ile	Asp	Leu	
85			90				95									
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg															336	
Arg	Gln	Met	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln	Gly	Gly	Cys	Gly	
100			105				110									
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc															384	
Ser	Cys	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	
115			120				125									
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac															432	
Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp	
130			135				140									
tgc gcc tcc caa cac gga cgt cat ggg gat acg att ccc aga ggt atc															480	
Cys	Ala	Ser	Gln	His	Gly	Arg	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile	
145			150				155								160	
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac															528	
Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr	
165			170				175									
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc															576	
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly	
180			185				190									
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg															624	
Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asn	Ala	Asn	Lys	Ile	Arg	
195			200				205									
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc															672	
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	
210			215				220									
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag															720	
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	
225			230				235								240	

cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt	768		
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly			
245	250	255	
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg	816		
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp			
260	265	270	
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc	864		
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile			
275	280	285	
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg	906		
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu			
290	295	300	
taa	909		
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<220>			
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<400> 11			
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn			
1	5	10	15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe			
20	25	30	
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His			
35	40	45	
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
 145 150 155 160
 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
 165 170 175
 Val Ala Arg Glu Gln Ser Arg Arg Arg Pro Asn Ala Gln Arg Phe Gly
 180 185 190
 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
 195 200 205
 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
 210 215 220
 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
 225 230 235 240
 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
 245 250 255
 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
 260 265 270
 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
 275 280 285
 Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
 290 295 300

<210> 12
 <211> 909
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)...(906)

<223> C103R mutant of ProDer p 1

<400> 12
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 Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1 5 10 15

a^a g^c a^gc t^at g^cc a^cc t^t c^t g^a g^a g^a g^cc g^c g^c a^a g^a a^ac t^t c⁹⁶
 Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
 20 25 30

ct^g g^aa a^gc g^tg a^{aa} t^ac g^tg c^ag a^ac g^gc g^gg g^ct a^ta a^at c^ac 144
 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
 35 40 45

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc	50	55	60	192
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser				
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	65	70	75	240
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu				
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	85	90	95	288
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu				
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	100	105	110	336
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly				
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	115	120	125	384
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu				
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	130	135	140	432
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp				
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	145	150	155	480
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile				
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	165	170	175	528
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr				
gta gct agg gag cag tcc cgt cgc cgt cct aac gca cag cgc ttc ggc	180	185	190	576
Val Ala Arg Glu Gln Ser Arg Arg Pro Asn Ala Gln Arg Phe Gly				
att tcc aat tat tgc cag atc tac ccc cct aat gcc aac aag atc agg	195	200	205	624
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg				
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	210	215	220	672
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile				
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	210	215	220	720
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln				

225	230	235	240	
				768
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly				
245	250	255		
				816
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp				
260	265	270		
				864
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc				
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile				
275	280	285		
				906
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg				
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu				
290	295	300		
taa				909
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<220>				
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<400> 13				
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Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe				
20	25	30		
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His				
35	40	45		
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser				
50	55	60		
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu				
65	70	75	80	
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu				
85	90	95		
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly				
100	105	110		
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu				
115	120	125		
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp				

130	135	140													
Cys	Ala	Ser	Gln	His	Gly	Cys	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile
145															160
Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr
															165
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly
															180
Ile	Ser	Asn	Tyr	Arg	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg
															195
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile
															210
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln
															225
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly
															245
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp
															260
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile
															275
Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu		
															290
															295
															300

<210> 14
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(906)

<223> C117R mutant of ProDer p 1

<400> 14

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1				5											15	

aag	agc	tat	gcc	acc	tcc	gag	gac	gag	gag	gcc	gcg	cgc	aag	aac	ttc	96
Lys	Ser	Tyr	Ala	Thr	Phe	Glu	Asp	Glu	Glu	Ala	Ala	Arg	Lys	Asn	Phe	
															20	
															25	
															30	

ctg	gaa	agc	gtg	aaa	tac	gtg	cag	agc	aac	ggc	ggg	gct	ata	aat	cac	144
Leu	Glu	Ser	Val	Lys	Tyr	Val	Gln	Ser	Asn	Gly	Gly	Ala	Ile	Asn	His	
															35	
															40	
															45	

ctg tcc gac ctg tct tta gac gag ttc aag aac cgg ttc ctg atg agc	192		
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser			
50	55	60	
gcc gag gct ttc gaa cac ctt aag acc cag ttt gat ctc aac gcg gag	240		
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu			
65	70	75	80
acc aac gcc tgc agt atc aac ggc aat gcc ccc gct gag att gat ctg	288		
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu			
85	90	95	
cgc cag atg agg acc gtg act ccc atc cgc atg caa ggc ggc tgc ggg	336		
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly			
100	105	110	
tct tgt tgg gcc ttt tca ggc gtg gcc gcg aca gag tcg gca tac ctc	384		
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu			
115	120	125	
gcg tat cgg aat cag agc ctg gac ctc gct gag cag gag ctc gtt gac	432		
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp			
130	135	140	
tgc gcc tcc caa cac gga tgt cat ggg gat acg att ccc aga ggt atc	480		
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile			
145	150	155	160
gaa tac atc cag cat aat ggc gtc gtg cag gaa agc tat tac cga tac	528		
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr			
165	170	175	
gta gct agg gag cag tcc tgc cgc cgt cct aac gca cag cgc ttc ggc	576		
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly			
180	185	190	
att tcc aat tat cgt cag atc tac ccc cct aat gcc aac aag atc agg	624		
Ile Ser Asn Tyr Arg Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg			
195	200	205	
gag gcc ctg gcg cag acg cac agc gcc atc gct gtc atc atc gga atc	672		
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile			
210	215	220	
aag gat ctg gac gca ttc cgg cac tat gac ggg cgc aca atc atc cag	720		

Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln	
225				230					235					240		
cgc gac aac gga tat cag cca aac tac cac gcg gtc aac atc gtg ggt															768	
Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly	
				245					250				255			
tac tcg aac gcc cag ggg gtg gac tac tgg atc gtg aga aac agt tgg															816	
Tyr	Ser	Asn	Ala	Gln	Gly	Val	Asp	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp	
				260					265				270			
gac act aac tgg ggc gac aac ggc tac ggc tac ttc gcc gcc aac atc															864	
Asp	Thr	Asn	Trp	Gly	Asp	Asn	Gly	Tyr	Gly	Tyr	Phe	Ala	Ala	Asn	Ile	
				275					280				285			
gac ctg atg atg atc gag gag tac ccg tac gtg gtg atc ctg															906	
Asp	Leu	Met	Met	Ile	Glu	Glu	Tyr	Pro	Tyr	Val	Val	Ile	Leu			
				290					295				300			
taa															909	
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<213> Artificial Sequence																
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ctgagattga tctgcgccag atgaggaccg tgactcccat ccgcattgc															108	
<210> 16																
<211> 103																
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cgatgggag tcacggtcct catctggcgc agatcaatct cagcggggc attgccgttgc															60	
atactacggg cgttggtctc cgcgttgaga tcgaaaactgg gtc															103	
<210> 17																

<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
caaggcggcc gtgggtcttg ttgggcctt tcaggcgtgg ccgcgcacaga gtcggcatac 60
ctcgcgtatc ggaatcagag cctggaccc tc 92

<210> 18
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
tcagcgaggt ccaggctctg attccgatac gcgaggtatg ccgactctgt cgccggccacg 60
cctgaaaagg cccacaaga cccacggccg cttgcatt 99

<210> 19
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
tgagcaggag ctcgttgacc gtgcctccca acacggatgt catgggata cgattccag 60
aggtatcgaa tacatccagc ata 83

<210> 20
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ctggatgtat tcgataacctc tggaaatcgt atccccatg acatccgtgt tggaggcac 60
ggtaaacgcg ctcctgc 77

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
actgacaggc ctcggccgag ctccattaa 29

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